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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

DECLARATION OF VISHWANATH R. IYER, Ph.D.  
UNDER 37 C.F.R. § 1.132

I, VISHWANATH R. IYER, Ph.D., declare and state as follows:

1. I am an Assistant Professor in the Section of Molecular Genetics and Microbiology, Institute of Cellular and Molecular Biology, University of Texas at Austin, where my laboratory currently studies global transcriptional control in yeast, gene expression programs during human cell proliferation, and genome-wide transcription factor targets in yeast and human. Immediately prior to this position, I spent four years as a postdoctoral fellow in the laboratory of Patrick O. Brown at Stanford University studying the transcriptional programs of yeast and of human cells. My *curriculum vitae* is attached hereto as Exhibit A.

2. Beginning in Dr. Brown's laboratory, where I helped to develop the first whole genome arrays for yeast and early versions of highly representative cDNA arrays for human cells, and continuing to the present day, I have used microarray-based gene expression analysis as a principal approach in much of my research.

3. Representative publications describing this work include:

DeRisi J. et al., "Exploring the metabolic and genetic control of gene expression on a genomic scale," *Science* 278:680-686 (1997);<sup>1</sup>

Marton et al., "Drug target validation and identification of secondary drug target effects using DNA microarrays," *Nature Med.* 4:1293-1301 (1998);<sup>2</sup>

Iyer et al., "The transcriptional program in the response of human fibroblasts to serum," *Science* 283:83-87 (1999);<sup>3</sup> and

Ross et al., "Systematic variation in gene expression patterns in human cancer cell lines," *Nature Genetics* 24: 227-235 (2000).<sup>4</sup>

Two of the papers describe our use of microarray-based expression profiling to explore the metabolic reprogramming that occurs during major physiological changes, both in yeast (DeRisi et al., during the shift from fermentation to respiration) and in human cells (Iyer et al., human fibroblasts exposed to serum). One reference describes our use of expression profile analysis in drug target validation and identification of secondary drug effects (Marton et al.). And one describes our use of expression profiling as a molecular phenotyping tool to discriminate among human cancer cells (Ross et al.).

4. Whether used to elucidate basic physiological responses, to study primary and secondary drug effects, or to discriminate and classify human cancers, expression profiling

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<sup>1</sup> Attached hereto as Exhibit B.

<sup>2</sup> Attached hereto as Exhibit C.

<sup>3</sup> Attached hereto as Exhibit D.

<sup>4</sup> Attached hereto as Exhibit E.

as we have practiced it relies for its power on comparison of patterns of expression.

5. For example, we have demonstrated that we can use the presence or absence of a characteristic drug "signature" pattern of altered gene expression in drug-treated cells to explore the mechanism of drug action, and to identify secondary effects that can signal potentially deleterious drug side effects. As another example, we have demonstrated that gene expression patterns can be used to classify human tumor cell lines. While it is of course advantageous to know the biological function of the encoded gene products in order to reach a better understanding of the cellular mechanisms underlying these results, these pattern-based analyses do not require knowledge of the biological function of the encoded proteins.

6. The resolution of the patterns used in such comparisons is determined by the number of genes detected: the greater the number of genes detected, the higher the resolution of the pattern. It goes without saying that higher resolution patterns are generally more useful in such comparisons than lower resolution patterns. With such higher resolutions comes a correspondingly higher degree of statistical confidence for distinguishing different patterns, as well as identifying similar ones.

7. Each gene included as a probe on a microarray provides a signal that is specific to the cognate transcript, at least to a first approximation.<sup>5</sup> Each new gene-specific

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<sup>5</sup> In a more nuanced view, it is certainly possible for a probe to signal the presence of a variety of splice variants of a single gene,  
(Continued...)

probe added to a microarray thus increases the number of genes detectable by the device, increasing the resolving power of the device. As I note above, higher resolution patterns are generally more useful in comparisons than lower resolution patterns. Accordingly, each new gene probe added to a microarray increases the usefulness of the device in gene expression profiling analyses. This proposition is so well-established as to be virtually an axiom in the art, and has been as long as I have been working in the field, and certainly since the time I embarked on the production of whole genome arrays in early 1996. Simply put, arrays with fewer gene-specific probes are inferior to arrays with more gene-specific probes.

8. For example, our ability to subdivide cancers into discriminable classes by expression profiling is limited by the resolution of the patterns produced. With more genes contributing to the expression patterns, we can potentially draw finer distinctions among the patterns, thus subdividing otherwise indistinguishable cancers into a greater number of classes; the greater the number of classes, the greater the likelihood that the cancers classified together will respond similarly to therapeutic intervention, permitting better individualization of therapy and, we hope, better treatment outcomes.

9. If a gene does not change expression in an experiment, or if a gene is not expressed and produces no

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(...Continued)

without discriminating among them, and for a probe to signal the presence of a variety of allelic variants of a single gene, again without discriminating among them.

signal in an experiment, that is not to say that the probe lacks usefulness on the array; it only means that an insufficient number of conditions have been sampled to identify expression changes. In fact, an experiment showing that a gene is not expressed or that its expression level does not change can be equally informative. To provide maximum versatility as a research tool, the microarray should include -- and as a biologist I would want my microarray to include -- each newly identified gene as a probe.

10. I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and may jeopardize the validity of any patent application in which this declaration is filed or any patent that issues thereon.

Vishwanath

October 20, 2003

VISHWANATH R. IYER, Ph.D.

Date